



## SEQUENCE LISTING #3

&lt;110&gt; Junghans, Richard P.

&lt;120&gt; Chimeric Effector Cell Receptors Against Carcinoembryonic Antigen

&lt;130&gt; 002

&lt;140&gt; 10/006,771

&lt;141&gt; 2001-12-10

&lt;150&gt; 60/250,090

&lt;151&gt; 2000-11-30

&lt;160&gt; 6

&lt;170&gt; PatentIn version 3.1

&lt;210&gt; 1

&lt;211&gt; 7654

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (2428)..(3759)

&lt;223&gt; Chimeric IgTCR sequence contained in retroviral vector. Retroviral vector sequence (non-coding regions) are incidental to the invention. The translated (coding region) is relevant to the invention. (pertinent to Figure 3.)

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tgaattatTTTAAAGTCATTCTTGTTAGGAAAGTACATTGGCACGTAAA	120
GGAGCCAAAGCAATCTGTGAAAGCCCAGGCTGGGAGCC	
CAGCAGTTGCATCCCTCC	180
TGGCGTGTACCTAAGGGTTCTTAATTGTG	
TGGTTCTAAATCTTCCAGA	240
GGGTTGTCTCATTCACTTC	
CACTTCGGTGCACAATACTT	300
GGACGCGGATTTACTGTCTT	
AGCATCTATCGGTGGCC	360
CGATTGAGGC	
TGAACCTGAGGCCACTTCT	420
TCAAGCTTGTAAAGAGAGAGCA	
CAAGCACCAGAAGAGGCTGA	480
CCCAGACCTGTTGGCATTTAACAAAGGGCTCCTGG	
GTCAGCTTGTGGAGCAGCTT	

cataagggtgc	aaatttagaaa	tataaataat	aagcccatat	caatttgtca	tctttttta	540
agctcaagtt	ttgaaagacc	ccacctgttag	gttggcaag	ctagcttaag	taacgccatt	600
ttgcaaggca	tggaaaatac	ataactgaga	atagagaagt	tcagatcaag	gttaggaaca	660
gagagacagc	agaatatggg	ccaaacagga	tatctgtgg	aagcagttcc	tgccccgctc	720
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aactgacgag	ttcgaacac	ccggccgcaa	ccctggaga	cgtcccagg	acttcggggg	1380
ccgttttgt	ggccgacct	gagtcctaaa	atcccgatcg	tttaggactc	tttggtgcac	1440
cccccttaga	ggagggat	gtgggtctgg	taggagacga	gaacctaaaa	cagttcccgc	1500
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gcagcatcgt	tctgtgtgt	ctctgtctga	ctgtgtttct	gtatttgtct	gaaaatatgg	1620
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ctgcagaatg	gccaacctt	aacgtcgat	ggccgcgaga	cggcacctt	aaccgagacc	1800
tcatcaccca	ggtaagatc	aaggtctttt	cacctggccc	gcatggacac	ccagaccagg	1860
tccctacat	cgtgacctgg	gaagccttgg	ctttgaccc	ccctccctgg	gtcaagccct	1920

## Chimeric Effector Cell Receptors Against ST25

ttgtacaccc	taaggctccg	cctcctcttc	ctccatccgc	cccgtctctc	ccccttgaac	1980
ctcctcggttc	gaccggcct	cgatcctccc	tttatccagc	cctcaactcct	tctcttaggcg	2040
cccccatatg	gccatatgag	atcttatatg	gggcacccccc	gccccttgta	aacttccctg	2100
accctgacat	gacaagagtt	actaacagcc	cctctctcca	agtcactta	caggcttcta	2160
cttagtccag	cacgaagtct	ggagacctct	ggcggcagcc	taccaagaac	aactggaccg	2220
accggtgtta	cctcaccctt	accgagtcgg	cgacacagtg	tgggtccgccc	gacaccagac	2280
taagaaccta	gaacctcgct	ggaaaggacc	ttacacagtc	ctgctgacca	cccccacccgc	2340
cctcaaagta	gacggcatcg	cagcttggat	acacgcccgc	cacgtgaagg	ctgcccaccc	2400
cgggggtgga	ccatcctcta	gactgcc	atg gga tgg	agc tgt atc atc	ctc ttc	2454
			Met Gly Trp	Ser Cys Ile Ile	Leu Phe	
			1	5		
ttg gta gca aca gct aca ggt gtc cac tcc gac atc cag ctg acc cag						2502
Leu Val Ala Thr Ala Thr Gly Val His Ser Asp Ile Gln Leu Thr Gln						
10	15	20	25			
agc cca agc agc ctg agc gcc agc gtg ggt gac aga gtg acc atc acc						2550
Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr						
30	35	40				
tgt aag gcc agt cag gat gtg ggt act tct gta gct tgg tac cag cag						2598
Cys Lys Ala Ser Gln Asp Val Gly Thr Ser Val Ala Trp Tyr Gln Gln						
45	50	55				
aag cca ggt aag gct cca aag ctg ctg atc tac tgg aca tcc acc cgg						2646
Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Trp Thr Ser Thr Arg						
60	65	70				
cac act ggt gtg cca agc aga ttc agc ggt agc ggt acc gac						2694
His Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Thr Asp						
75	80	85				
ttc acc ttc acc atc agc agc ctc cag cca gag gac atc gcc acc tac						2742
Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr						
90	95	100	105			
tac tgc cag caa tat agc ctc tat cgg tcg ttc ggc caa ggg acc aag						2790
Tyr Cys Gln Gln Tyr Ser Leu Tyr Arg Ser Phe Gly Gln Gly Thr Lys						
110	115	120				

## Chimeric Effector Cell Receptors Against ST25

gtg gaa atc aaa cga ggt ggc tca gga tcg ggt gga tcc ggc tct ggt Val Glu Ile Lys Arg Gly Gly Ser Gly Ser Gly Gly Ser Gly Ser Gly 125 130 135	2838
ggc tca gga tcg gag gtc caa ctg gtg gag agc ggt gga ggt gtt gtg Gly Ser Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Val Val 140 145 150	2886
caa cct ggc cgg tcc ctg cgc ctg tcc tgc tcc gca tct ggc ttc gat Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ser Ala Ser Gly Phe Asp 155 160 165	2934
ttc acc aca tat tgg atg agt tgg gtg aga cag gca cct gga aaa ggt Phe Thr Thr Tyr Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly 170 175 180 185	2982
ctt gag tgg att gga gaa att cat cca gat agc agt acg att aac tat Leu Glu Trp Ile Gly Glu Ile His Pro Asp Ser Ser Thr Ile Asn Tyr 190 195 200	3030
gcg ccg tct cta aag gat aga ttt aca ata tcg cga gac aac gcc aag Ala Pro Ser Leu Lys Asp Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys 205 210 215	3078
aac aca ttg ttc ctg caa atg gac agc ctg aga ccc gaa gac acc ggg Asn Thr Leu Phe Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly 220 225 230	3126
gtc tat ttt tgt gca agc ctt tac ttc ggc ttc ccc tgg ttt gct tat Val Tyr Phe Cys Ala Ser Leu Tyr Phe Gly Phe Pro Trp Phe Ala Tyr 235 240 245	3174
tgg ggc caa ggg acc ccg gtc acc gtc tcc agt gct aag ccc acc acg Trp Gly Gln Gly Thr Pro Val Thr Val Ser Ser Ala Lys Pro Thr Thr 250 255 260 265	3222
acg cca gcg ccg cga cca aca ccg gcg ccc acc atc gcg tcg cag Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln 270 275 280	3270
ccc ctg tcc ctg cgc cca gag gcg gct cggt cca gcg gcg ggg ggc gca Pro Leu Ser Leu Arg Pro Glu Ala Ala Arg Pro Ala Ala Gly Gly Ala 285 290 295	3318
gtg cac acg agg ggg ctg gac ttc gcc ctg gat ccc aaa ctc tgc tac Val His Thr Arg Gly Leu Asp Phe Ala Leu Asp Pro Lys Leu Cys Tyr 300 305 310	3366

ctg ctg gat gga atc ctc ttc atc tat ggt gtc att ctc act gcc ttg Leu Leu Asp Gly Ile Leu Phe Ile Tyr Gly Val Ile Leu Thr Ala Leu 315                   320                   325	3414
ttc ctg aga gtg aag ttc agc agg agc gca gag ccc ccc gcg tac cag Phe Leu Arg Val Lys Phe Ser Arg Ser Ala Glu Pro Pro Ala Tyr Gln 330                   335                   340                   345	3462
cag ggc cag aac cag ctc tat aac gag ctc aat cta gga cga aga gag Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu 350                   355                   360	3510
gag tac gat gtt ttg gac aag aga cgt ggc cg <sup>g</sup> gac cct gag atg ggg Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly 365                   370                   375	3558
gga aag ccg aga agg aag aac cct cag gaa ggc ctg tac aat gaa ctg Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu 380                   385                   390	3606
cag aaa gat aag atg gcg gag gcc tac agt gag att ggg atg aaa ggc Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly 395                   400                   405	3654
gag cgc cg <sup>g</sup> agg ggc aag ggg cac gat ggc ctt tac cag ggt ctc agt Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser 410                   415                   420                   425	3702
aca gcc acc aag gac acc tac gac gcc ctt cac atg cag gcc ctg ccc Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro 430                   435                   440	3750
cct cgc taa ctcgacgcgg ccgcggatcc ggattagtcc aatttgttaa Pro Arg	3799
agacaggata tcagtggtcc aggctctagt tttgactcaa caatatcacc agctgaagcc	3859
tataaggtac gagccataga taaaataaaa gattttattt agtctccaga aaaagggggg	3919
aatgaaagac cccacctgta ggttggcaa gctagctaa gtaacgccat tttgcaaggc	3979
atggaaaata cataactgag aatagagaag ttcagatcaa ggttaggaac agagagacag	4039
cagaatatgg gccaaacagg atatctgtgg taagcagttc ctgccccgct cagggccaag	4099
aacagttgga acaggagaat atgggc当地 caggatatct gtggtaagca gttcctgccc	4159

cggctcagg ccaagaacag atggtcccc gatgcggtcc cgccctcagc agtttctaga	4219
gaaccatcag atgttccag ggtgcccaa ggacctgaaa tgaccctgtg ccttatttga	4279
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aaagagccc caaccctca ctgcggcgc cagtcctccg atagactgcf tcgcccgggt	4399
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acgacggcca gtgcc	7654

<210> 2  
<211> 443  
<212> PRT  
<213> Homo sapiens

<400> 2

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly			
1	5	10	15
10	15		

Val His Ser Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala			
20	25	30	
30			

Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Val			
35	40	45	
45			

Gly Thr Ser Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys			
50	55	60	
60			

Leu Leu Ile Tyr Trp Thr Ser Thr Arg His Thr Gly Val Pro Ser Arg

Chimeric Effector Cell Receptors Against ST25

65

70

75

80

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser  
85 90 95

Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Leu  
100 105 110

Tyr Arg Ser Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Gly Gly  
115 120 125

Ser Gly Ser Gly Gly Ser Gly Ser Gly Ser Gly Ser Glu Val Gln  
130 135 140

Leu Val Glu Ser Gly Gly Val Val Gln Pro Gly Arg Ser Leu Arg  
145 150 155 160

Leu Ser Cys Ser Ala Ser Gly Phe Asp Phe Thr Thr Tyr Trp Met Ser  
165 170 175

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile Gly Glu Ile  
180 185 190

His Pro Asp Ser Ser Thr Ile Asn Tyr Ala Pro Ser Leu Lys Asp Arg  
195 200 205

Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Phe Leu Gln Met  
210 215 220

Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys Ala Ser Leu  
225 230 240

Tyr Phe Gly Phe Pro Trp Phe Ala Tyr Trp Gly Gln Gly Thr Pro Val  
245 250 255

Thr Val Ser Ser Ala Lys Pro Thr Thr Pro Ala Pro Arg Pro Pro

260

265

270

Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu  
275 280 285

Ala Ala Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp  
290 295 300

Phe Ala Leu Asp Pro Lys Leu Cys Tyr Leu Leu Asp Gly Ile Leu Phe  
305 310 315 320

Ile Tyr Gly Val Ile Leu Thr Ala Leu Phe Leu Arg Val Lys Phe Ser  
325 330 335

Arg Ser Ala Glu Pro Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr  
340 345 350

Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys  
355 360 365

Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn  
370 375 380

Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu  
385 390 395 400

Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly  
405 410 415

His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr  
420 425 430

Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg  
435 440

&lt;210&gt; 3

<211> 422  
<212> DNA  
<213> Homo sapiens and Mus sp.

<220>  
<221> CDS  
<222> (8)..(421)  
<223> hMn14 VH, humanized (CDR-grafted) anti-CEA antibody heavy chain V region (aa20-138) with leader (aa1-19) (pertinent to Fig. 4A.)

<400> 3		
cctcacc atg gga tgg agc tgt atc atc ctc ttc ttg gta gca aca gct		49
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala		
1 5 10		
aca ggt gtc cac tcc gag gtc caa ctg gtg gag agc ggt gga ggt gtt		97
Thr Gly Val His Ser Glu Val Gln Leu Val Glu Ser Gly Gly Val		
15 20 25 30		
gtg caa cct ggc cg <sup>g</sup> tcc ctg cgc ctg tcc tgc tcc gca tct ggc ttc		145
Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ser Ala Ser Gly Phe		
35 40 45		
gat ttc acc aca tat tgg atg agt tgg gtg aga cag gca cct gga aaa		193
Asp Phe Thr Thr Tyr Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys		
50 55 60		
ggt ctt gag tgg att gga gaa att cat cca gat agc agt acg att aac		241
Gly Leu Glu Trp Ile Gly Glu Ile His Pro Asp Ser Ser Thr Ile Asn		
65 70 75		
tat gcg ccg tct cta aag gat aga ttt aca ata tcg cga gac aac gcc		289
Tyr Ala Pro Ser Leu Lys Asp Arg Phe Thr Ile Ser Arg Asp Asn Ala		
80 85 90		
aag aac aca ttg ttc ctg caa atg gac agc ctg aga ccc gaa gac acc		337
Lys Asn Thr Leu Phe Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr		
95 100 105 110		
ggg gtc tat ttt tgt gca agc ctt tac ttc ggc ttc ccc tgg ttt gct		385
Gly Val Tyr Phe Cys Ala Ser Leu Tyr Phe Gly Phe Pro Trp Phe Ala		
115 120 125		
tat tgg ggc caa ggg acc ccg gtc acc gtc tcc tca g		422
Tyr Trp Gly Gln Gly Thr Pro Val Thr Val Ser Ser		
130 135		

Chimeric Effector Cell Receptors Against ST25

<210> 4  
<211> 138  
<212> PRT  
<213> Homo sapiens and Mus sp.

<400> 4

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly  
1 5 10 15

Val His Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln  
20 25 30

Pro Gly Arg Ser Leu Arg Leu Ser Cys Ser Ala Ser Gly Phe Asp Phe  
35 40 45

Thr Thr Tyr Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu  
50 55 60

Glu Trp Ile Gly Glu Ile His Pro Asp Ser Ser Thr Ile Asn Tyr Ala  
65 70 75 80

Pro Ser Leu Lys Asp Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn  
85 90 95

Thr Leu Phe Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val  
100 105 110

Tyr Phe Cys Ala Ser Leu Tyr Phe Gly Phe Pro Trp Phe Ala Tyr Trp  
115 120 125

Gly Gln Gly Thr Pro Val Thr Val Ser Ser  
130 135

<210> 5  
<211> 712  
<212> DNA  
<213> Homo sapiens and Mus sp.

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (14)..(712)

&lt;223&gt; hMN14 VLCK, humanized (CDR-grafted) anti-CEA antibody kappa light chain V region (aa20-126), with human constant CK domain (aa127-232) and leader (aa1-19). (pertinent to Figure 4B.)

&lt;400&gt; 5

tctagaccc	acc	atg	gga	tgg	agc	tgt	atc	atc	ctc	ttc	ttg	gta	gca	49		
		Met	Gly	Trp	Ser	Cys	Ile	Ile	Leu	Phe	Leu	Val	Ala			
		1					5					10				
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Thr	Ala	Thr	Gly	Val	His	Ser	Asp	Ile	Gln	Leu	Thr	Gln	Ser	Pro	Ser	
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Ser	Leu	Ser	Ala	Ser	Val	Gly	Asp	Arg	Val	Thr	Ile	Thr	Cys	Lys	Ala	
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agt	cag	gat	gtg	ggt	act	tct	gta	gct	tgg	tac	cag	cag	aag	cca	193	
Ser	Gln	Asp	Val	Gly	Thr	Ser	Val	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	
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aag	gct	cca	aag	ctg	ctg	atc	tac	tgg	aca	tcc	acc	cgg	cac	act	241	
Lys	Ala	Pro	Lys	Leu	Leu	Ile	Tyr	Trp	Thr	Ser	Thr	Arg	His	Thr	Gly	
65						70			75							
gtg	cca	agc	aga	ttc	agc	ggt	agc	ggt	acc	gac	ttc	acc	ttc		289	
Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Phe	
80					85					90						
acc	atc	agc	agc	ctc	cag	cca	gag	gac	atc	gcc	acc	tac	tac	tgc	337	
Thr	Ile	Ser	Ser	Leu	Gln	Pro	Glu	Asp	Ile	Ala	Thr	Tyr	Tyr	Cys	Gln	
95					100					105						
caa	tat	agc	ctc	tat	cg	tcg	ttc	ggc	caa	ggg	acc	aag	gtg	gaa	atc	385
Gln	Tyr	Ser	Leu	Tyr	Arg	Ser	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	
110					115					120						
aaa	cga	act	gtg	gct	gca	cca	tct	gtc	ttc	atc	ttc	ccg	cca	tct	433	
Lys	Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	
125						130				135			140			
gag	cag	ttg	aaa	tct	gga	act	gcc	tct	gtt	gtg	tgc	ctg	ctg	aat	aac	481
Glu	Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	

145	150	155	
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caa tcg ggt aac tcc cag gag agt gtc aca gag cag gac agc aag gac Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp 175	180	185	577
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gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag ggc ctg agc Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser 205	210	215	673
tcg ccc gtc aca aag agc ttc aac agg gga gag tgt taa Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys 225	230		712
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Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Val 35	40	45	
Gly Thr Ser Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys 50	55	60	
Leu Leu Ile Tyr Trp Thr Ser Thr Arg His Thr Gly Val Pro Ser Arg 65	70	75	80

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser  
85 90 95

Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Leu  
100 105 110

Tyr Arg Ser Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val  
115 120 125

Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys  
130 135 140

Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg  
145 150 155 160

Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn  
165 170 175

Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser  
180 185 190

Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys  
195 200 205

Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr  
210 215 220

Lys Ser Phe Asn Arg Gly Glu Cys  
225 230